CLAIMS

1. Method for identifying and selecting a gene required for the proliferation *in vivo* of a pathogenic microorganism, comprising :

- using a strain of the pathogenic microorganism,
- generating mutants for inactivation in the genes encoding these factors,
- determining the virulence of these mutants on an experimental model of infection, and their effect on enteric colonization in an axenic mouse model, and
- selecting the bacterial genes essential for resistance to serum *in vitro*, and essential, in the host, for dissemination in the serum.

2. Method according to Claim 1, characterized by the use of an *E.coli* strain EXPEC or a *Streptococcus agalactiae* strain.

3. Mutant nucleic acids for inactivation of the virulence genes as implemented in the method according to Claim 1 or 2.

4. Mutant nucleic acids which are sensitive to serum; avirulent in mice model and able to colonize gut of axenic mice.

5. Pathogenicity or virulence targets encoded by isolated or purified nucleic acids corresponding to one of the nucleotide sequences SEQ ID Nos 16-30.

6. Pathogenicity or virulence targets according to claim 5, wherein said nucleic acids correspond to one of the nucleotide sequences SEQ ID Nos 16,17,19-30.

7. Pathogenicity or virulence targets according to claim 5 or 6, wherein said nucleic acids are cDNAs.

8. Pathogenicity or virulence targets according to claim 5 or 6, wherein said nucleic acids are RNAs.

9. Pathogenicity or virulence targets according to any one of claims 6 to 8, wherein said nuclesic acids correspond to the nucleic acids of pathogenic organisms comprising *Escherichia coli, Salmonella typhimurium, Klebsiella pneumoniae, Yersinia pestis, Serratia marcescens, Haemophilus influenzae, Pasteurella multocida, Vibrio cholerae, Pseudomonas aeruginosa, Acetinobacter, Moraxella catarrhalis, Burkholderia pseudomallei, Neisseria meningitidis, Neisseria gonorrhoeae, Campylobacter jejuni, Helicobacter pylori, Bacteroides fragilis, Clostridium acetobutylicum, Mycobacterium tuberculosis, Streptococcus pyogenes, Streptococcus agalactiae, Staphyloccus aureus* and *Enterococcus*.

10. Pathogenicity or virulence targets according to claim 9 corresponding to nucleic acids of *E.coli* or *Streptococcus agalactiae*.

11. Vectors comprising at least one pathogenicity or virulence target according to any one of claims 5 to 10.

12. Host cells containing at least one vector according to Claim 11.

13. Products of expression of the pathogenicity or virulence targets according to any one of claims 5 to 10.

14. Isolated or purified peptides characterized in that they correspond to one of the amino acid sequences SEQ ID Nos. 1 to 15.

15. Isolated or purified peptides according to claim 14 characterized in that they correspond to one of the amino acid sequences SEQ ID Nos 1,2,4-15.

16. Antibodies capable of binding specifically to the peptides according to any one of Claims 13 to 15.

17. Method for inhibiting *in vitro* the proliferation of a pathogenic microorganism in serum, comprising the use of an effective amount of a compound capable of inhibiting the activity, or of reducing the amount, of pathogenicity or virulence target according to any one of claims 6 to 10, or of inhibiting the activity of a peptide according to Claim 15.

18. Method for screening compounds capable of inhibiting the expression of the pathogenicity or virulence target according to any one of claims 6 to 10, or peptides according to claim 15, comprising bringing into contact with the test compound, demonstrating the possible effect of the compound on their activity, and selecting the active compounds.

19. Method for screening compounds capable of inhibiting the biochemical and/or enzyme activity of the peptides expressed by the pathogenicity or virulence target according to any one of claims 6 to 10.

20. Use of the compounds selected according to Claim 19, for developing medicinal products for inhibiting a bacterial infection, in particular an extra-intestinal infection in the case of enterobacteria.